

PTO/PCT Rec'd



#5

SEQUENCE LISTING

<11	0 > No	orth	west	Bio	ther	apeu	tics	, In	c.						
<12	120> METHODS FOR THE DIAGNOSIS AND TREATMENT OF METASTATIC PROSTATE TUMORS														
<13	<130> 8511-025-228														
	40> PCT/US99/08079 41> 1999-04-13														
<16	0> 1	б													
<17	0 > Pa	aten	tIn '	Ver.	2.0										
<21 <21	<210> 1 <211> 4450 <212> DNA <213> Homo sapiens														
<22	0 > 1 > C	ns													
		22).	. (39	15)											
<pre><400> 1 acccacgcgc agcggccgga g atg cag cgg ggc gcc gcg ctg tgc ctg cga 5 Met Gln Arg Gly Ala Ala Leu Cys Leu Arg</pre>												51			
					gga Gly										99
					ttg Leu										147
					tcc Ser										195
					gct Ala										243
					gtg Val 80										291
					ttg Leu										339
					tac Tyr										387

_	_	_	_	tcc Ser				_	-			_		435
		_		gac Asp	-	_	_			_	_	_	_	483
				gtg Val 160										531
				ctg Leu										579
				ctc Leu										627
-	_	_		acc Thr		 	_	_	_					675
				atc Ile										723
				ctg Leu 240										771
				gct Ala										819
				cag Gln										867
				cac His										915
				gac Asp										963
				cgg Arg 320										1011
				gag Glu										1059

gca Ala																1107
ccg Pro																1155
cac His																1203
ggc Gly 395																1251
aac Asn		_	_		_				_			_				1299
aag Lys																1347
ctc Leu		_	_	_					_			_		_		1395
cac His																1443
cgg Arg 475																1491
gcg Ala			_	-	_	_						_	_	_		1539
tgg Trp							_		_			_	_	_		1587
atc Ile																1635
aag Lys																1683
ccc Pro 555																1731
ggc	cag	ccg	gtg	ctc	ctg	agc	tgc	caa	gcc	gac	agc	tac	aag	tac	gag	1779

	Gly	Gln	Pro	Val	Leu 575	Leu	Ser	Cys	Gln	Ala 580	Asp	Ser	Tyr	Lys	Tyr 585	Glu	
							ctc Leu										1827
÷							gac Asp										1875
							gag Glu 625										1923
							ccc Pro										1971
-							gac Asp										2019
-							cag Gln										2067
							gtg Val										2115
							cac His 705										2163
			_	_			aag Lys			_	_	_		_			2211
							cgc Arg										2259
							ccc Pro										2307
							gag Glu										2355
							atc Ile 785										2403
							agg Arg										2451

•

795	800	805	810
Gly Tyr Leu Ser I		ccc ggg gag gtg cct Pro Gly Glu Val Pro 820	
	eu Ser Tyr Asp	gcc agc cag tgg gaa Ala Ser Gln Trp Glu 835	
		ctc ggc tac ggc gcc Leu Gly Tyr Gly Ala 855	
		atc cac aag ggc agc Ile His Lys Gly Ser 870	
		gag ggc gcc acg gcc Glu Gly Ala Thr Ala 885	
Arg Ala Leu Met S		atc ctc att cac atc Ile Leu Ile His Ile 900	
	sn Leu Leu Gly	gcg tgc acc aag ccg Ala Cys Thr Lys Pro 915	
		aag tac ggc aac ctc Lys Tyr Gly Asn Leu 935	
		agc ccc tgc gcg gag Ser Pro Cys Ala Glu 950	
		atg gtg gag ctc gcc Met Val Glu Leu Ala . 965	
Arg Arg Arg Pro G		agg gtc ctc ttc gcg Arg Val Leu Phe Ala . 980	
	y Ala Arg Arg	gct tct cca gac caa Ala Ser Pro Asp Gln 995	
		atg gaa gat ctt gtc Met Glu Asp Leu Val 1015	-
		ttc ctg gct tcc cga Phe Leu Ala Ser Arg 1030	

His Arg Asp Leu Ala	Ala Arg Asn Ile Leu	ctg tcg gaa agc gac gtg Leu Ser Glu Ser Asp Val 045 1050	3171
		gac atc tac aaa gac ccc Asp Ile Tyr Lys Asp Pro 1065	3219
		ccc ctg aag tgg atg gcc Pro Leu Lys Trp Met Ala 1080	3267
		acg cag agt gac gtg tgg Thr Gln Ser Asp Val Trp 1095	3315
		tct ctg ggg gcc tcc ccg Ser Leu Gly Ala Ser Pro 1110	3363
Tyr Pro Gly Val Gln	Ile Asn Glu Glu Phe	tgc cag cgc gtg aga gac Cys Gln Arg Val Arg Asp 125 1130	3411
		act ccc gcc ata cgc cac Thr Pro Ala Ile Arg His 1145	3459
		aag gcg aga cct gca ttc Lys Ala Arg Pro Ala Phe 1160	3507
		ctc cag ggc agg ggc ctg Leu Gln Gly Arg Gly Leu 1175	3555
		cgc agc tct cag agc tca Arg Ser Ser Gln Ser Ser 1190	3603
Glu Glu Gly Ser Phe	Ser Gln Val Ser Thr	atg gcc cta cac atc gcc Met Ala Leu His Ile Ala 205 1210	3651
		ctg cag cgc cac agc ctg Leu Gln Arg His Ser Leu 1225	3699
		ccc ggg tgc ctg gcc aga Pro Gly Cys Leu Ala Arg 1240	3747
		aag aca ttt gag gaa ttc Lys Thr Phe Glu Glu Phe 1255	3795

.

3843 ccc atg acc cca acg acc tac aaa ggc tct gtg gac aac cag aca gac Pro Met Thr Pro Thr Tyr Lys Gly Ser Val Asp Asn Gln Thr Asp 1260 1265 3891 agt ggg atg gtg ctg gcc tcg gag gag ttt gag cag ata gag agc agg Ser Gly Met Val Leu Ala Ser Glu Glu Phe Glu Gln Ile Glu Ser Arg 1280 1285 cat aga caa gaa agc ggc ttc agg tagctgaagc agagagagag aaggcagcat His Arg Gln Glu Ser Gly Phe Arg 1295 acqtcaqcat tttcttctct qcacttataa qaaagatcaa agactttaag actttcgcta 4005 tttcttctac tgctatctac tacaaacttc aaagaggaac caggaggaca agaggagcat 4065 gaaagtggac aaggagtgtg accactgaag caccacaggg aggggttagg cctccggatg 4125 actgcgggca ggcctggata atatccagcc tcccacaaga agctggtgga gcagagtgtt 4185 ccctgactcc tccaaggaaa gggagacgcc ctttcatggt ctgctgagta acaggtgcct 4245 teccaqaeae tqqcqttact qettqaecaa aqaqeeetca ageggeeett atgccagegt 4305 gacagagggc teaectettg cettetaggt caetteteae aatgteeett cageacetga 4365 ccctgtgccc gccgattatt ccttggtaat atgagtaata catcaaagag tagtattaaa 4425 4450 agctaattaa tcatgtttat aaaaa <210> 2 <211> 1298 <212> PRT <213> Homo sapiens <400> 2 Met Gln Arg Gly Ala Ala Leu Cys Leu Arg Leu Trp Leu Cys Leu Gly 5 Leu Leu Asp Gly Leu Val Ser Asp Tyr Ser Met Thr Pro Pro Thr Leu Asn Ile Thr Glu Glu Ser His Val Ile Asp Thr Gly Asp Ser Leu Ser 40 Ile Ser Cys Arg Gly Gln His Pro Leu Glu Trp Ala Trp Pro Gly Ala 50 Gln Glu Ala Pro Ala Thr Gly Asp Lys Asp Ser Glu Asp Thr Gly Val Val Arg Asp Cys Glu Gly Thr Asp Ala Arg Pro Tyr Cys Lys Val Leu

Leu Leu His Glu Val His Ala Asn Asp Thr Gly Ser Tyr Val Cys Tyr

105

110

_		_		_		_	-1	~ 1	~ 1	1	_,	47 .		~	_
Tyr	гуѕ	1yr 115	lle	гÀв	Ala	Arg	11e 120	Glu	GIY	Tnr	Tnr	125	Ala	ser	ser
Tyr	Val 130	Phe	Val	Arg	Asp	Phe 135	Glu	Gln	Pro	Phe	Ile 140	Asn	Lys	Pro	Asp
Thr 145	Leu	Leu	Val	Asn	Arg 150	Lys	Asp	Ala	Met	Trp 155	Val	Pro	Cys	Leu	Val 160
Ser	Ile	Pro	Gly	Leu 165	Asn	Val	Thr	Leu	Arg 170	Ser	Gln	Ser	Ser	Val 175	Leu
Trp	Pro	Asp	Gly 180	Gln	Glu	Val	Val	Trp 185	Asp	Asp	Arg	Arg	Gly 190	Met	Leu
Val	Ser	Thr 195	Pro	Leu	Leu	His	Asp 200	Ala	Leu	Tyr	Leu	Gln 205	Cys	Glu	Thr
Thr	Trp 210	Gly	Asp	Gln	Asp	Phe 215	Leu	Ser	Asn	Pro	Phe 220	Leu	Val	His	Ile
Thr 225	Gly	Asn	Glu	Leu	Tyr 230	Asp	Ile	Gln	Leu	Leu 235	Pro	Arg	Lys	Ser	Leu 240
Glu	Leu	Leu	Val	Gly 245	Glu	Lys	Leu	Val	Leu 250	Asn	Cys	Thr	Val	Trp 255	Ala
Glu	Phe	Asn	Ser 260	Gly	Val	Thr	Phe	Asp 265	Trp	Asp	Tyr	Pro	Gly 270	Lys	Gln
Ala	Glu	Arg 275	Gly	Lys	Trp	Val	Pro 280	Glu	Arg	Arg	Ser	Gln 285	Gln	Thr	His
Thr	Glu 290	Leu	Ser	Ser	Ile	Leu 295	Thr	Ile	His	Asn	Val 300	Ser	Gln	His	Asp
Leu 305	Gly	Ser	Tyr	Val	Cys 310	Lys	Ala	Asn	Asn	Gly 315	Ile	Gln	Arg	Phe	Arg 320
Glu	Ser	Thr	Glu	Val 325	Ile	Val	His	Glu	Asn 330	Pro	Phe	Ile	Ser	Val 335	Glu
Trp	Leu	Lys	Gly 340	Pro	Ile	Leu	Glu	Ala 345	Thr	Ala	Gly	Asp	Glu 350	Leu	Val
Lys	Leu	Pro 355	Val	Lys	Leu	Ala	Ala 360	Tyr	Pro	Pro	Pro	Glu 365	Phe	Gln	Trp
Tyr	Lys 370	Asp	Gly	Lys	Ala	Leu 375	Ser	Gly	Arg	His	Ser 380	Pro	His	Ala	Leu
Val 385	Leu	Lys	Glu	Val	Thr 390	Glu	Ala	Ser	Thr	Gly 395	Thr	Tyr	Thr	Leu	Ala 400
Leu	Trp	Asn	Ser	Ala 405	Ala	Gly	Leu	Arg	Arg 410	Asn	Ile	Ser	Leu	Glu 415	Leu

•

Val	Val	Asn	Val 420	Pro	Pro	Gln	Ile	His 425	Glu	Lys	Glu	Ala	Ser 430	Ser	Pro
Ser	Ile	Tyr 435	Ser	Arg	His	Ser	Arg 440	Gln	Ala	Leu	Thr	Cys 445	Thr	Ala	Tyr
Gly	Val 450	Pro	Leu	Pro	Leu	Ser 455	Ile	Gln	Trp	His	Trp 460	Arg	Pro	Trp	Thr
Pro 465	Cys	Lys	Met	Phe	Ala 470	Gln	Arg	Ser	Leu	Arg 475	Arg	Arg	Gln	Gln	Gln 480
Asp	Leu	Met	Pro	Gln 485	Cys	Arg	Asp	Trp	Arg 490	Ala	Val	Thr	Thr	Gln 495	Asp
Ala	Val	Asn	Pro 500	Ile	Glu	Ser	Leu	Asp 505	Thr	Trp	Thr	Glu	Phe 510	Val	Glu
Gly	Lys	Asn 515	Lys	Thr	Val	Ser	Lys 520	Leu	Val	Ile	Gln	Asn 525	Ala	Asn	Val
Ser	Ala 530	Met	Tyr	Lys	Cys	Val 535	Val	Ser	Asn	Lys	Val 540	Gly	Gln	Asp	Glu
Arg 545	Leu	Ile	Tyr	Phe	Tyr 550	Val	Thr	Thr	Ile	Pro 555	Asp	Gly	Phe	Thr	Ile 560
Glu	Ser	Lys	Pro	Ser 565	Glu	Glu	Leu	Leu	Glu 570	Gly	Gln	Pro	Val	Leu 575	Leu
Ser	Cys	Gln	Ala 580		Ser	Tyr	Lys	Tyr 585	Glu	His	Leu	Arg	Trp 590	Tyr	Arg
Leu	Asn	Leu 595	Ser	Thr	Leu	His	Asp 600	Ala	His	Gly	Asn	Pro 605	Leu	Leu	Leu
Asp	Cys 610	Lys	Asn	Val	His	Leu 615	Phe	Ala	Thr	Pro	Leu 620	Ala	Ala	Ser	Leu
Glu 625	Glu	Val	Ala	Pro	Gly 630	Ala	Arg	His	Ala	Thr 635	Leu	Ser	Leu	Ser	Ile 640
Pro	Arg	Val	Ala	Pro 645	Glu	His	Glu	Gly	His 650	Tyr	Val	Cys	Glu	Val 655	Gln
Asp	Arg	Arg	Ser 660	His	Asp	Lys	His	Cys 665	His	Lys	Lys	Tyr	Leu 670	Ser	Val
Gln	Ala	Leu 675	Glu	Ala	Pro	Arg	Leu 680	Thr	Gln	Asn	Leu	Thr 685	Asp	Leu	Leu
Val	Asn 690	Val	Ser	Asp	Ser	Leu 695	Glu	Met	Gln	Сув	Leu 700	Val	Ala	Gly	Ala
His 705	Ala	Pro	Ser	Ile	Val 710	Trp	Tyr	Lys	Asp	Glu 715	Arg	Leu	Leu	Glu	Glu 720

- Lys Ser Gly Val Asp Leu Ala Asp Ser Asn Gln Lys Leu Ser Ile Gln 725 730 735
- Arg Val Arg Glu Glu Asp Ala Gly Pro Tyr Leu Cys Ser Val Cys Arg
 740 745 750
- Pro Lys Gly Cys Val Asn Ser Ser Ala Ser Val Ala Val Glu Gly Ser 755 760 765
- Glu Asp Lys Gly Ser Met Glu Ile Val Ile Leu Val Gly Thr Gly Val 770 780
- Ile Ala Val Phe Phe Trp Val Leu Leu Leu Ile Phe Cys Asn Met 785 790 795 800
- Arg Arg Pro Ala His Ala Asp Ile Lys Thr Gly Tyr Leu Ser Ile Ile 805 810 815
- Met Asp Pro Gly Glu Val Pro Leu Glu Glu Gln Cys Glu Tyr Leu Ser 820 825 830
- Tyr Asp Ala Ser Gln Trp Glu Phe Pro Arg Glu Arg Leu His Leu Gly 835 840 845
- Arg Val Leu Gly Tyr Gly Ala Phe Gly Lys Val Val Glu Ala Ser Ala 850 855 860
- Phe Gly Ile His Lys Gly Ser Ser Cys Asp Thr Val Ala Val Lys Met 865 870 875 880
- Leu Lys Glu Gly Ala Thr Ala Ser Glu Gln Arg Ala Leu Met Ser Glu 885 890 895
- Leu Lys Ile Leu Ile His Ile Gly Asn His Leu Asn Val Val Asn Leu 900 905 910
- Leu Gly Ala Cys Thr Lys Pro Gln Gly Pro Leu Met Val Ile Val Glu 915 920 925
- Phe Cys Lys Tyr Gly Asn Leu Ser Asn Phe Leu Arg Ala Lys Arg Asp 930 935 940
- Ala Phe Ser Pro Cys Ala Glu Lys Ser Pro Glu Gln Arg Gly Arg Phe 945 950 955 960
- Arg Ala Met Val Glu Leu Ala Arg Leu Asp Arg Arg Pro Gly Ser 965 970 975
- Ser Asp Arg Val Leu Phe Ala Arg Phe Ser Lys Thr Glu Gly Gly Ala 980 985 990
- Arg Arg Ala Ser Pro Asp Gln Glu Ala Glu Asp Leu Trp Leu Ser Pro
 995 1000 1005
- Leu Thr Met Glu Asp Leu Val Cys Tyr Ser Phe Gln Val Ala Arg Gly
 1010 1015 1020

Met Glu Phe Leu Ala Ser Arg Lys Cys Ile His Arg Asp Leu Ala Ala 025 1030 1035 1040

Arg Asn Ile Leu Leu Ser Glu Ser Asp Val Val Lys Ile Cys Asp Phe 1045 1050 1055

Gly Leu Ala Arg Asp Ile Tyr Lys Asp Pro Asp Tyr Val Arg Lys Gly
1060 1065 1070

Ser Ala Arg Leu Pro Leu Lys Trp Met Ala Pro Glu Ser Ile Phe Asp 1075 1080 1085

Lys Val Tyr Thr Thr Gln Ser Asp Val Trp Ser Phe Gly Val Leu Leu 1090 1095 1100

Trp Glu Ile Phe Ser Leu Gly Ala Ser Pro Tyr Pro Gly Val Gln Ile 105 1110 1115 1120

Asn Glu Glu Phe Cys Gln Arg Val Arg Asp Gly Thr Arg Met Arg Ala 1125 1130 1135

Pro Glu Leu Ala Thr Pro Ala Ile Arg His Ile Met Leu Asn Cys Trp 1140 1145 1150

Ser Gly Asp Pro Lys Ala Arg Pro Ala Phe Ser Asp Leu Val Glu Ile 1155 1160 1165

Leu Gly Asp Leu Leu Gln Gly Arg Gly Leu Gln Glu Glu Glu Val 1170 1175 1180

Cys Met Ala Pro Arg Ser Ser Gln Ser Ser Glu Glu Gly Ser Phe Ser 185 1190 1195 1200

Gln Val Ser Thr Met Ala Leu His Ile Ala Gln Ala Asp Ala Glu Asp 1205 1210 1215

Ser Pro Pro Ser Leu Gln Arg His Ser Leu Ala Ala Arg Tyr Tyr Asn 1220 1230

Trp Val Ser Phe Pro Gly Cys Leu Ala Arg Gly Ala Glu Thr Arg Gly 1235 1240 1245

Ser Ser Arg Met Lys Thr Phe Glu Glu Phe Pro Met Thr Pro Thr Thr 1250 1255 1260

Tyr Lys Gly Ser Val Asp Asn Gln Thr Asp Ser Gly Met Val Leu Ala 265 1270 1275 1280

Ser Glu Glu Phe Glu Gln Ile Glu Ser Arg His Arg Gln Glu Ser Gly 1285 1290 1295

Phe Arg

```
<211> 15
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence:
      oligonucleotide
<400> 3
ggcgccccgc tgcat
                                                                     15
<210> 4
<211> 23
<212> DNA
<213> Artificial Sequence
<223> Description of Artificial Sequence: primer
<400> 4
cgaagtggtg aagttcatgg atg
                                                                    23
<210> 5
<211> 25
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: primer
<400> 5
ttctgtatca gtctttcctg gtgag
                                                                    25
<210> 6
<211> 24
<212> DNA
<213> Artificial Sequence
<223> Description of Artificial Sequence: primer
<400> 6
ctggcatggt cttctgtgaa agca
                                                                    24
<210> 7
<211> 22
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: primer
<400> 7
```

```
aataccagtg gatgtgatgc gg
                                                                     22
 <210> 8
 <211> 20
 <212> DNA
 <213> Artificial Sequence
 <223> Description of Artificial Sequence: primer
<400> 8
 taccacagtg tcaggcagcg
                                                                     20
 <210> 9
 <211> 20
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: primer
<400> 9
 atcaaattct cggttggccc
                                                                     20
 <210> 10
 <211> 20
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: primer
 <400> 10
 agagggatgg agttcctggc
                                                                     20
 <210> 11
 <211> 22
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: primer
 <400> 11
 aataccagtg gatgtgatgc gg
                                                                     22
 <210> 12
 <211> 21
 <212> DNA
 <213> Artificial Sequence
```

<220>

<223> Description of Artificial oligonucleotide	Sequence:	
<400> 12 agacagcaga aagttcatgg t		21
<210> 13 <211> 15 <212> DNA <213> Artificial Sequence		
<220> <223> Description of Artificial oligonucleotide	Sequence:	
<400> 13 caagtgcatg gtgga		15
<210> 14 <211> 15 <212> DNA <213> Artificial Sequence		
<220> <223> Description of Artificial oligonucleotide	Sequence:	
<400> 14 caccttgctc tgcat		15
<210> 15 <211> 14 <212> DNA <213> Artificial Sequence		
<220> <223> Description of Artificial oligonucleotide	Sequence:	
<400> 15 cccggtgtcc caga		14
<210> 16 <211> 17 <212> DNA <213> Artificial Sequence		
<220> <223> Description of Artificial oligonucleotide	Sequence:	
<400> 16 tacgtagtat ggtgtac		17